

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/506,666

Source:

PET

Date Processed by STIC:

6/3/05

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PCT

RAW SEQUENCE LISTING

DATE: 06/03/2005

PATENT APPLICATION: US/10/506,666

TIME: 10:25:24

Input Set : A:\seq list.txt

Output Set: N:\CRF4\06032005\J506666.raw

3 <110> APPLICANT: ESCAICH, Sonia
 5 <120> TITLE OF INVENTION: New Products Specific to Pathogenic Strains and Their
 6 Use as Vaccines and in Immunotherapy
 8 <130> FILE REFERENCE: 1721-81
 10 <140> CURRENT APPLICATION NUMBER: 10/506,666
 C--> 11 <141> CURRENT FILING DATE: 2004-09-07
 13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/02925
 14 <151> PRIOR FILING DATE: 2003-03-06
 16 <150> PRIOR APPLICATION NUMBER: EP02290556.6
 17 <151> PRIOR FILING DATE: 2002-03-06
 19 <160> NUMBER OF SEQ ID NOS: 158
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 163
 25 <212> TYPE: PRT
 27 <213> ORGANISM: Escherichia coli
 30 <400> SEQUENCE: 1
 32 Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile
 33 1 5 10 15
 36 Val Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Asn
 37 20 25 30
 40 Val Leu Gln Arg Thr Cys Asn Val Pro Gly Asn Val Asp Val Ser Leu
 41 35 40 45
 44 Gly Asn Leu Tyr Val Ser Asp Phe Pro Asn Ala Gly Ser Gly Ser Pro
 45 50 55 60
 48 Trp Val Asn Phe Asp Leu Ser Leu Thr Gly Cys Gln Asn Met Asn Thr
 49 65 70 75 80
 52 Val Arg Ala Thr Phe Ser Gly Thr Ala Asp Gly Gln Thr Tyr Tyr Ala
 53 85 90 95
 56 Asn Thr Gly Asn Ala Gly Gly Ile Lys Ile Glu Ile Gln Asp Arg Asp
 57 100 105 110
 60 Gly Ser Asn Ala Ser Tyr His Asn Gly Met Phe Lys Thr Leu Asn Val
 61 115 120 125
 64 Gln Asn Asn Asn Ala Thr Phe Asn Leu Lys Ala Arg Ala Val Ser Lys
 65 130 135 140
 68 Gly Gln Val Thr Pro Gly Asn Ile Ser Ser Val Ile Thr Val Thr Tyr
 69 145 150 155 160
 72 Thr Tyr Ala
 76 <210> SEQ ID NO: 2
 77 <211> LENGTH: 673
 78 <212> TYPE: PRT
 80 <213> ORGANISM: Escherichia coli
 83 <400> SEQUENCE: 2

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85 Met Lys Met Thr Arg Leu Tyr Pro Leu Ala Leu Gly Gly Leu Leu Leu
86 1          5          10          15
89 Pro Ala Ile Ala Asn Ala Gln Thr Ser Gln Gln Asp Glu Ser Thr Leu
90          20          25          30
93 Val Val Thr Ala Ser Lys Gln Ser Ser Arg Ser Ala Ser Ala Asn Asn
94          35          40          45
97 Val Ser Ser Thr Val Val Ser Ala Pro Glu Leu Ser Asp Ala Gly Val
98          50          55          60
101 Thr Ala Ser Asp Lys Leu Pro Arg Val Leu Pro Gly Leu Asn Ile Glu
102 65          70          75          80
105 Asn Ser Gly Asn Met Leu Phe Ser Thr Ile Ser Leu Arg Gly Val Ser
106          85          90          95
109 Ser Ala Gln Asp Phe Tyr Asn Pro Ala Val Thr Leu Tyr Val Asp Gly
110          100          105          110
113 Val Pro Gln Leu Ser Thr Asn Thr Ile Gln Ala Leu Thr Asp Val Gln
114          115          120          125
117 Ser Val Glu Leu Leu Arg Gly Pro Gln Gly Thr Leu Tyr Gly Lys Ser
118          130          135          140
121 Ala Gln Gly Gly Ile Ile Asn Ile Val Thr Gln Gln Pro Asp Ser Thr
122 145          150          155          160
125 Pro Arg Gly Tyr Ile Glu Gly Gly Val Ser Ser Arg Asp Ser Tyr Arg
126          165          170          175
129 Ser Lys Phe Asn Leu Ser Gly Pro Ile Gln Asp Gly Leu Leu Tyr Gly
130          180          185          190
133 Ser Val Thr Leu Leu Arg Gln Val Asp Asp Gly Asp Met Ile Asn Pro
134          195          200          205
137 Ala Thr Gly Ser Asp Asp Leu Gly Gly Thr Arg Ala Ser Ile Gly Asn
138          210          215          220
141 Val Lys Leu Arg Leu Ala Pro Asp Asp Gln Pro Trp Glu Met Gly Phe
142 225          230          235          240
145 Ala Ala Ser Arg Glu Cys Thr Arg Ala Thr Gln Asp Ala Tyr Val Gly
146          245          250          255
149 Trp Asn Asp Ile Lys Gly Arg Lys Leu Ser Ile Ser Asp Gly Ser Pro
150          260          265          270
153 Asp Pro Tyr Met Arg Arg Cys Thr Asp Ser Gln Thr Leu Ser Gly Lys
154          275          280          285
157 Tyr Thr Thr Asp Asp Trp Val Phe Asn Leu Ile Ser Ala Trp Gln Gln
158          290          295          300
161 Gln His Tyr Ser Arg Thr Phe Pro Ser Gly Ser Leu Ile Val Asn Met
162 305          310          315          320
165 Ser Gln Arg Trp Asn Gln Asp Val Gln Glu Leu Arg Ala Ala Thr Leu
166          325          330          335
169 Gly Asp Ala Arg Thr Val Asp Met Val Phe Gly Leu Tyr Arg Gln Asn
170          340          345          350
173 Thr Arg Glu Lys Leu Asn Ser Ala Tyr Asp Met Pro Thr Met Pro Tyr
174          355          360          365
177 Leu Ser Ser Thr Gly Tyr Thr Thr Ala Glu Thr Leu Ala Ala Tyr Ser
178          370          375          380
181 Asp Leu Thr Trp His Leu Thr Asp Arg Phe Asp Ile Gly Gly Gly Val

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182 385          390          395          400
185 Arg Phe Ser His Asp Lys Ser Ser Thr Gln Tyr His Gly Ser Met Leu
186          405          410          415
189 Gly Asn Pro Phe Gly Asp Gln Gly Lys Ser Asn Asp Asp Gln Val Leu
190          420          425          430
193 Gly Gln Leu Ser Ala Gly Tyr Met Leu Thr Asp Asp Trp Arg Val Tyr
194          435          440          445
197 Thr Arg Val Ala Gln Gly Tyr Lys Pro Ser Gly Tyr Asn Ile Val Pro
198          450          455          460
201 Thr Ala Gly Leu Asp Ala Lys Pro Phe Val Ala Glu Lys Ser Ile Asn
202 465          470          475          480
205 Tyr Glu Leu Gly Thr Arg Tyr Glu Thr Ala Asp Val Thr Leu Gln Ala
206          485          490          495
209 Ala Thr Phe Tyr Thr His Thr Lys Asp Met Gln Leu Tyr Ser Gly Pro
210          500          505          510
213 Val Gly Met Gln Thr Leu Ser Asn Ala Gly Lys Ala Asp Ala Thr Gly
214          515          520          525
217 Val Glu Leu Glu Ala Lys Trp Arg Phe Ala Pro Gly Trp Ser Trp Asp
218          530          535          540
221 Ile Asn Gly Asn Val Ile Arg Ser Glu Phe Thr Asn Asp Ser Glu Leu
222 545          550          555          560
225 Tyr His Gly Asn Arg Val Pro Phe Val Pro Arg Tyr Gly Ala Gly Ser
226          565          570          575
229 Ser Val Asn Gly Val Ile Asp Thr Arg Tyr Gly Ala Leu Met Pro Arg
230          580          585          590
233 Leu Ala Val Asn Leu Val Gly Pro His Tyr Phe Asp Gly Asp Asn Gln
234          595          600          605
237 Leu Arg Gln Gly Thr Tyr Ala Thr Leu Asp Ser Ser Leu Gly Trp Gln
238          610          615          620
241 Ala Thr Glu Arg Met Asn Ile Ser Val Tyr Val Asp Asn Leu Phe Asp
242 625          630          635          640
245 Arg Arg Tyr Arg Thr Tyr Gly Tyr Met Asn Gly Ser Ser Ala Val Ala
246          645          650          655
250 Gln Val Asn Met Gly Arg Thr Val Gly Ile Asn Thr Arg Ile Asp Phe
251          660          665          670
254 Phe
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 246
260 <212> TYPE: PRT
261 <213> ORGANISM: Escherichia coli
263 <400> SEQUENCE: 3
265 Met Asn Lys Val Phe Val Val Ser Val Val Ala Ala Ala Cys Val Phe
266 1          5          10          15
269 Ala Val Asn Ala Gly Ala Lys Glu Gly Lys Ser Gly Phe Tyr Leu Thr
270          20          25          30
273 Gly Lys Ala Gly Ala Ser Val Met Ser Leu Ser Asp Gln Arg Phe Leu
274          35          40          45
277 Ser Gly Asp Glu Glu Glu Thr Ser Lys Tyr Lys Gly Gly Asp Asp His
278          50          55          60

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281 Asp Thr Val Phe Ser Gly Gly Ile Ala Val Gly Tyr Asp Phe Tyr Pro
282 65              70              75              80
285 Gln Phe Ser Ile Pro Val Arg Thr Glu Leu Glu Phe Tyr Ala Arg Gly
286              85              90              95
289 Lys Ala Asp Ser Lys Tyr Asn Val Asp Lys Asp Ser Trp Ser Gly Gly
290              100             105             110
293 Tyr Trp Arg Asp Asp Leu Lys Asn Glu Val Ser Val Asn Thr Leu Met
294              115             120             125
297 Leu Asn Ala Tyr Tyr Asp Phe Arg Asn Asp Ser Ala Phe Thr Pro Trp
298              130             135             140
301 Val Ser Ala Gly Ile Gly Tyr Ala Arg Ile His Gln Lys Thr Thr Gly
302 145              150              155              160
305 Ile Ser Thr Trp Asp Tyr Glu Tyr Gly Ser Ser Gly Arg Glu Ser Leu
306              165              170              175
309 Ser Arg Ser Gly Ser Ala Asp Asn Phe Ala Trp Ser Leu Gly Ala Gly
310              180             185             190
313 Val Arg Tyr Asp Val Thr Pro Asp Ile Ala Leu Asp Leu Ser Tyr Arg
314              195             200             205
317 Tyr Leu Asp Ala Gly Asp Ser Ser Val Ser Tyr Lys Asp Glu Trp Gly
318              210             215             220
321 Asp Lys Tyr Lys Ser Glu Val Asp Val Lys Ser His Asp Ile Met Leu
322 225              230             235             240
325 Gly Met Thr Tyr Asn Phe
326              245
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 166
331 <212> TYPE: PRT
333 <213> ORGANISM: Escherichia coli
335 <400> SEQUENCE: 4
337 Met Lys Leu Lys Ala Ile Ile Leu Ala Thr Gly Leu Ile Asn Cys Ile
338 1              5              10              15
341 Ala Phe Ser Ala Gln Ala Val Asp Thr Thr Ile Thr Val Thr Gly Arg
342              20              25              30
345 Val Leu Pro Arg Thr Cys Thr Ile Gly Asn Gly Gly Asn Pro Asn Ala
346              35              40              45
349 Thr Val Val Leu Asp Asn Ala Tyr Thr Ser Asp Leu Ile Ala Ala Asn
350              50              55              60
353 Ser Thr Ser Gln Trp Lys Asn Phe Ser Leu Thr Leu Thr Asn Cys Gln
354 65              70              75              80
357 Asn Val Asn Asn Val Thr Ser Phe Gly Gly Thr Ala Glu Asn Thr Asn
358              85              90              95
361 Tyr Tyr Arg Asn Thr Gly Asp Ala Thr Asn Ile Met Val Glu Leu Gln
362              100             105             110
365 Glu Gln Gly Asn Gly Asn Thr Pro Leu Lys Val Gly Ser Thr Lys Val
366              115             120             125
369 Val Thr Val Ser Asn Gly Gln Ala Thr Phe Asn Leu Lys Val Arg Ala
370              130             135             140
373 Val Ser Lys Gly Asn Ala Gly Ala Gly Ser Ile Asn Ser Gln Ile Thr
374 145             150             155             160

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377 Val Thr Tyr Thr Tyr Ala
378                               165
381 <210> SEQ ID NO: 5
382 <211> LENGTH: 1295
383 <212> TYPE: PRT
385 <213> ORGANISM: Escherichia coli
387 <400> SEQUENCE: 5
389 Met Asn Lys Ile Tyr Ser Leu Lys Tyr Ser Ala Ala Thr Gly Gly Leu
390 1                               5                               10                               15
393 Ile Ala Val Ser Glu Leu Ala Lys Arg Val Ser Gly Lys Thr Asn Arg
394                               20                               25                               30
397 Lys Leu Val Ala Thr Met Leu Ser Leu Ala Val Ala Gly Thr Val Asn
398                               35                               40                               45
401 Ala Ala Asn Ile Asp Ile Ser Asn Val Trp Ala Arg Asp Tyr Leu Asp
402                               50                               55                               60
405 Leu Ala Gln Asn Lys Gly Ile Phe Gln Pro Gly Ala Thr Asp Val Thr
406 65                               70                               75                               80
409 Ile Thr Leu Lys Asn Gly Asp Lys Phe Ser Phe His Asn Leu Ser Ile
410                               85                               90                               95
413 Pro Asp Phe Ser Gly Ala Ala Ala Ser Gly Ala Ala Thr Ala Ile Gly
414                               100                              105                              110
417 Gly Ser Tyr Ser Val Thr Val Ala His Asn Lys Lys Asn Pro Gln Ala
418                               115                              120                              125
421 Ala Glu Thr Gln Val Tyr Ala Gln Ser Ser Tyr Arg Val Val Asp Arg
422                               130                              135                              140
426 Arg Asn Ser Asn Asp Phe Glu Ile Gln Arg Leu Asn Lys Phe Val Val
427 145                              150                              155                              160
430 Glu Thr Val Gly Ala Thr Pro Ala Glu Thr Asn Pro Thr Thr Tyr Ser
431                               165                              170                              175
434 Asp Ala Leu Glu Arg Tyr Gly Ile Val Thr Ser Asp Gly Ser Lys Lys
435                               180                              185                              190
438 Ile Ile Gly Phe Arg Ala Gly Ser Gly Gly Thr Ser Phe Ile Asn Gly
439                               195                              200                              205
442 Glu Ser Lys Ile Ser Thr Asn Ser Ala Tyr Ser His Asp Leu Leu Ser
443                               210                              215                              220
446 Ala Ser Leu Phe Glu Val Thr Gln Trp Asp Ser Tyr Gly Met Met Ile
447 225                              230                              235                              240
450 Tyr Lys Asn Asp Lys Thr Phe Arg Asn Leu Glu Ile Phe Gly Asp Ser
451                               245                              250                              255
454 Gly Ser Gly Ala Tyr Leu Tyr Asp Asn Lys Leu Glu Lys Trp Val Leu
455                               260                              265                              270
458 Val Gly Thr Thr His Gly Ile Ala Ser Val Asn Gly Asp Gln Leu Thr
459                               275                              280                              285
462 Trp Ile Thr Lys Tyr Asn Asp Lys Leu Val Ser Glu Leu Lys Asp Thr
463                               290                              295                              300
466 Tyr Ser His Lys Ile Asn Leu Asn Gly Asn Asn Val Thr Ile Lys Asn
467 305                              310                              315                              320
470 Thr Asp Ile Thr Leu His Gln Asn Asn Ala Asp Thr Thr Gly Thr Gln
471                               325                              330                              335

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date